

25
SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Lobb, Roy R.; Burkly, Linda C.
- (ii) TITLE OF INVENTION: Treatment for Asthma
- 10 (iii) NUMBER OF SEQUENCES: 11
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: LAHIVE & COCKFIELD
- (B) STREET: 60 State Street, Suite 510
- (C) CITY: Boston
- 15 (D) STATE: Massachusetts
- (E) COUNTRY: USA
- (F) ZIP: 02109-1875
- (v) COMPUTER READABLE FORM:
- 20 (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- 25 (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (vii) PRIOR APPLICATION DATA:
- 30 (A) APPLICATION NUMBER: US 08/374,331
- (B) FILING DATE: 18-JAN-1995
- (vii) PRIOR APPLICATION DATA:
- 35 (A) APPLICATION NUMBER: US 08/256,631
- (B) FILING DATE: 12-JUL-1994
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: PCT/US93/00030
- (B) FILING DATE: 12-JAN-1993
- 40 (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: US 07/821,768
- (B) FILING DATE: 13-JAN 1992
- 45 (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Myers, Louis (PLM)
- (B) REGISTRATION NUMBER: 35,965
- (C) REFERENCE/DOCKET NUMBER: BGP-021USCP2
- 50 (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (617)227-7400
- (B) TELEFAX: (617)227-5941

55 (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 360 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

10 (B) LOCATION: 1..360

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1

15 (D) OTHER INFORMATION: /note= "pBAG159 insert: HP1/2 heavy
 chain variable region; amino acid 1 is Glu (E) but
 Gln (Q) may be substituted"

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| GTC | AAA | CTG | CAG | CAG | TCT | GGG | GCA | GAG | CTT | GTG | AAG | CCA | GGG | GCC | TCA | 48 |
| Val | Lys | Leu | Gln | Gln | Ser | Gly | Ala | Glu | Leu | Val | Lys | Pro | Gly | Ala | Ser | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| GTC | AAG | TTG | TCC | TGC | ACA | GCT | TCT | GGC | TTC | AAC | ATT | AAA | GAC | ACC | TAT | 96 |
| Val | Lys | Leu | Ser | Cys | Thr | Ala | Ser | Gly | Phe | Asn | Ile | Lys | Asp | Thr | Tyr | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | CAC | TGG | GTG | AAG | CAG | AGG | CCT | GAA | CAG | GGC | CTG | GAG | TGG | ATT | GGA | 144 |
| Met | His | Trp | Val | Lys | Gln | Arg | Pro | Glu | Gln | Gly | Leu | Glu | Trp | Ile | Gly | |
| | | 35 | | | | 40 | | | | 45 | | | | | | |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AGG | ATT | GAT | CCT | GCG | AGT | GGC | GAT | ACT | AAA | TAT | GAC | CCG | AAG | TTC | CAG | 192 |
| Arg | Ile | Asp | Pro | Ala | Ser | Gly | Asp | Thr | Lys | Tyr | Asp | Pro | Lys | Phe | Gln | |
| | 50 | | | | | 55 | | | | 60 | | | | | | |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GTC | AAG | GCC | ACT | ATT | ACA | GCG | GAC | ACG | TCC | TCC | AAC | ACA | GCC | TGG | CTG | 240 |
| Val | Lys | Ala | Thr | Ile | Thr | Ala | Asp | Thr | Ser | Ser | Asn | Thr | Ala | Trp | Leu | |
| 40 | 65 | | | | 70 | | | | 75 | | | | | 80 | | |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CAG | CTC | AGC | AGC | CTG | ACA | TCT | GAG | GAC | ACT | GCC | GTC | TAC | TAC | TGT | GCA | 288 |
| Gln | Leu | Ser | Ser | Leu | Thr | Ser | Glu | Asp | Thr | Ala | Val | Tyr | Tyr | Cys | Ala | |
| | | | 85 | | | | 90 | | | | | | | 95 | | |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GAC | GGA | ATG | TGG | GTA | TCA | ACG | GGA | TAT | GCT | CTG | GAC | TTC | TGG | GGC | CAA | 336 |
| Asp | Gly | Met | Trp | Val | Ser | Thr | Gly | Tyr | Ala | Leu | Asp | Phe | Trp | Gly | Gln | |
| | | | 100 | | | | 105 | | | | | | 110 | | | |

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|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|--|--|--|-----|
| GGG | ACC | ACG | GTC | ACC | GTC | TCC | TCA | | | | | | | | | 360 |
| Gly | Thr | Thr | Val | Thr | Val | Ser | Ser | | | | | | | | | |
| | | | 115 | | | 120 | | | | | | | | | | |

55 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
1 5 10 15
Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
20 25 30
Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
15 35 40 45
Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
50 55 60
Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
20 65 70 75 80
Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95
Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
100 105 110
Gly Thr Thr Val Thr Val Ser Ser
115 120

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

45 (A) NAME/KEY: CDS
(B) LOCATION: 1..318
(D) OTHER INFORMATION: /note= "HP1/2 light chain variable
region"

(ix) FEATURE:

50 (A) NAME/KEY: misc_feature
(B) LOCATION: 1
(D) OTHER INFORMATION: /note= "pBAG172 insert: HP1/2 light
chain variable region"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGT ATT GTG ATG ACC CAG ACT CCC AAA TTC CTG CTT GTT TCA GCA GGA

28

Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
1 5 10 15

5 GAC AGG GTT ACC ATA ACC TGC AAG GCC AGT CAG AGT GTG ACT AAT GAT 96
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
20 25 30

10 GTA GCT TGG TAC CAA CAG AAG CCA GGG CAG TCT CCT AAA CTG CTG ATA 144
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

TAT TAT GCA TCC AAT CGC TAC ACT GGA GTC CCT GAT CGC TTC ACT GGC 192
Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

15 AGT GGA TAT GGG ACG GAT TTC ACT TTC ACC ATC AGC ACT GTG CAG GCT 240
Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
65 70 75 80

20 GAA GAC CTG GCA GTT TAT TTC TGT CAG CAG GAT TAT AGC TCT CCG TAC 288
Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
85 90 95

25 ACG TTC GGA GGG GGG ACC AAG CTG GAG ATC 318
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
100 105

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

40 Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
20 25 30

45 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

50 Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
65 70 75 80

55 Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile

2) INFORMATION FOR SEQ ID NO: 5:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

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(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1338

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(ix) FEATURE:

- (A) NAME/KEY: VCAM-1 gene segment
- (B) LOCATION: 1..219
- (D) OTHER INFORMATION: This portion of the sequence corresponds, in part, to Exons I, II and III nucleotide sequence of Cybulsky et al. Proc. Nat'l. Acad. Sci. USA 88: 7861(1991).

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(ix) FEATURE:

- (A) NAME/KEY: Hinge region
- (B) LOCATION: 220..229
- (D) OTHER INFORMATION: This portion of the sequence corresponds, in part, to Fig. 12A in PCT/US92/02050 and represents the hinge region of Human IgG1 heavy chain constant region.

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(ix) FEATURE:

- (A) NAME/KEY: Heavy chain constant region 2
- (B) LOCATION: 230..338
- (D) OTHER INFORMATION: This portion of the sequence corresponds, in part, to Fig. 12A in PCT/US92/02050 and represents the heavy chain constant region 2 of Human IgG1 heavy chain constant region.

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(ix) FEATURE:

- (A) NAME/KEY: Heavy chain constant region 3
- (B) LOCATION: 339..446
- (D) OTHER INFORMATION: This portion of the sequence corresponds, in part, to Fig. 12A in PCT/US92/02050 and represents the heavy chain constant region 3 of Human IgG1 heavy chain constant region.

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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ATG CCT GGG AAG ATG GTC GTG ATC CTT GGA GCC TCA AAT ATA CTT TGG
 Met Pro Gly Lys Met Val Val Ile Leu Gly Ala Ser Asn Ile Leu Trp
 110 115 120 125

48

ATA ATG TTT GCA GCT TCT CAA GCT TTT AAA ATC GAG ACC ACC CCA GAA

96

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|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | Ile | Met | Phe | Ala | Ala | Ser | Gln | Ala | Phe | Lys | Ile | Glu | Thr | Thr | Pro | Glu | |
| | | | | | 130 | | | | | 135 | | | | | 140 | | |
| 5 | TCT | AGA | TAT | CTT | GCT | CAG | ATT | GGT | GAC | TCC | GTC | TCA | TTG | ACT | TGC | AGC | 144 |
| | Ser | Arg | Tyr | Leu | Ala | Gln | Ile | Gly | Asp | Ser | Val | Ser | Leu | Thr | Cys | Ser | |
| | | | | 145 | | | | 150 | | | | | 155 | | | | |
| 10 | ACC | ACA | GGC | TGT | GAG | TCC | CCA | TTT | TTC | TCT | TGG | AGA | ACC | CAG | ATA | GAT | 192 |
| | Thr | Thr | Gly | Cys | Glu | Ser | Pro | Phe | Phe | Ser | Trp | Arg | Thr | Gln | Ile | Asp | |
| | | | 160 | | | | | 165 | | | | | 170 | | | | |
| 15 | AGT | CCA | CTG | AAT | GGG | AAG | GTG | ACG | AAT | GAG | GGG | ACC | ACA | TCT | ACG | CTG | 240 |
| | Ser | Pro | Leu | Asn | Gly | Lys | Val | Thr | Asn | Glu | Gly | Thr | Thr | Ser | Thr | Leu | |
| | | 175 | | | | | 180 | | | | | 185 | | | | | |
| 20 | ACA | ATG | AAT | CCT | GTT | AGT | TTT | GGG | AAC | GAA | CAC | TCT | TAC | CTG | TGC | ACA | 288 |
| | Thr | Met | Asn | Pro | Val | Ser | Phe | Gly | Asn | Glu | His | Ser | Tyr | Leu | Cys | Thr | |
| | 190 | | | | | 195 | | | | | 200 | | | | | 205 | |
| 25 | GCA | ACT | TGT | GAA | TCT | AGG | AAA | TTG | GAA | AAA | GGA | ATC | CAG | GTG | GAG | ATC | 336 |
| | Ala | Thr | Cys | Glu | Ser | Arg | Lys | Leu | Glu | Lys | Gly | Ile | Gln | Val | Glu | Ile | |
| | | | | 210 | | | | | | 215 | | | | | 220 | | |
| 30 | TAC | TCT | TTT | CCT | AAG | GAT | CCA | GAG | ATT | CAT | TTG | AGT | GGC | CCT | CTG | GAG | 384 |
| | Tyr | Ser | Phe | Pro | Lys | Asp | Pro | Glu | Ile | His | Leu | Ser | Gly | Pro | Leu | Glu | |
| | | | | 225 | | | | | 230 | | | | | 235 | | | |
| 35 | GCT | GGG | AAG | CCG | ATC | ACA | GTC | AAG | TGT | TCA | GTT | GCT | GAT | GTA | TAC | CCA | 432 |
| | Ala | Gly | Lys | Pro | Ile | Thr | Val | Lys | Cys | Ser | Val | Ala | Asp | Val | Tyr | Pro | |
| | | | 240 | | | | | 245 | | | | | 250 | | | | |
| 40 | TTT | GAC | AGG | CTG | GAG | ATA | GAC | TTA | CTG | AAA | GGA | GAT | CAT | CTC | ATG | AAG | 480 |
| | Phe | Asp | Arg | Leu | Glu | Ile | Asp | Leu | Leu | Lys | Gly | Asp | His | Leu | Met | Lys | |
| | | 255 | | | | | 260 | | | | | 265 | | | | | |
| 45 | AGT | CAG | GAA | TTT | CTG | GAG | GAT | GCA | GAC | AGG | AAG | TCC | CTG | GAA | ACC | AAG | 528 |
| | Ser | Gln | Glu | Phe | Leu | Glu | Asp | Ala | Asp | Arg | Lys | Ser | Leu | Glu | Thr | Lys | |
| | | 270 | | | | 275 | | | | | 280 | | | | | 285 | |
| 50 | AGT | TTG | GAA | GTA | ACC | TTT | ACT | CCT | GTC | ATT | GAG | GAT | ATT | GGA | AAA | GTT | 576 |
| | Ser | Leu | Glu | Val | Thr | Phe | Thr | Pro | Val | Ile | Glu | Asp | Ile | Gly | Lys | Val | |
| | | | | | 290 | | | | | 295 | | | | | 300 | | |
| 55 | CTT | GTT | TGC | CGA | GCT | AAA | TTA | CAC | ATT | GAT | GAA | ATG | GAT | TCT | GTG | CCC | 624 |
| | Leu | Val | Cys | Arg | Ala | Lys | Leu | His | Ile | Asp | Glu | Met | Asp | Ser | Val | Pro | |
| | | | | 305 | | | | | 310 | | | | | 315 | | | |
| 60 | ACA | GTA | AGG | CAG | GCT | GTA | AAA | GAA | TTG | CAA | GTC | GAC | AAA | ACT | CAC | ACA | 672 |
| | Thr | Val | Arg | Gln | Ala | Val | Lys | Glu | Leu | Gln | Val | Asp | Lys | Thr | His | Thr | |
| | | | 320 | | | | | 325 | | | | | 330 | | | | |
| 65 | TGC | CCA | CCG | TGC | CCA | GCA | CCT | GAA | CTC | CTG | GGG | GGA | CCG | TCA | GTC | TTC | 720 |
| | Cys | Pro | Pro | Cys | Pro | Ala | Pro | Glu | Leu | Leu | Gly | Gly | Pro | Ser | Val | Phe | |
| | | | 335 | | | | 340 | | | | | 345 | | | | | |
| 70 | CTC | TTC | CCC | CCA | AAA | CCC | AAG | GAC | ACC | CTC | ATG | ATC | TCC | CGG | ACC | CCT | 768 |
| | Leu | Phe | Pro | Pro | Lys | Pro | Lys | Asp | Thr | Leu | Met | Ile | Ser | Arg | Thr | Pro | |
| | | | | | | 355 | | | | | 360 | | | | | 365 | |

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|----|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| | GAG | GTC | ACA | TGC | GTG | GTG | GTG | GAC | GTG | AGC | CAC | GAA | GAC | CCT | GAG | GTC | 816 |
| | Glu | Val | Thr | Cys | Val | Val | Val | Asp | Val | Ser | His | Glu | Asp | Pro | Glu | Val | |
| | | | | | 370 | | | | | 375 | | | | | 380 | | |
| 5 | AAG | TTC | AAC | TGG | TAC | GTG | GAC | GGC | GTG | GAG | GTG | CAT | AAT | GCC | AAG | ACA | 864 |
| | Lys | Phe | Asn | Trp | Tyr | Val | Asp | Gly | Val | Glu | Val | His | Asn | Ala | Lys | Thr | |
| | | | | 385 | | | | | 390 | | | | | 395 | | | |
| 10 | AAG | CCG | CGG | GAG | GAG | CAG | TAC | AAC | AGC | ACG | TAC | CGG | GTG | GTC | AGC | GTC | 912 |
| | Lys | Pro | Arg | Glu | Glu | Gln | Tyr | Asn | Ser | Thr | Tyr | Arg | Val | Val | Ser | Val | |
| | | | 400 | | | | | 405 | | | | | 410 | | | | |
| 15 | CTC | ACC | GTC | CTG | CAC | CAG | GAC | TGG | CTG | AAT | GGC | AAG | GAG | TAC | AAG | TGC | 960 |
| | Leu | Thr | Val | Leu | His | Gln | Asp | Trp | Leu | Asn | Gly | Lys | Glu | Tyr | Lys | Cys | |
| | | 415 | | | | | 420 | | | | | 425 | | | | | |
| 20 | AAG | GTC | TCC | AAC | AAA | GCC | CTC | CCA | GCC | CCC | ATC | GAG | AAA | ACC | ATC | TCC | 1008 |
| | Lys | Val | Ser | Asn | Lys | Ala | Leu | Pro | Ala | Pro | Ile | Glu | Lys | Thr | Ile | Ser | |
| | 430 | | | | | 435 | | | | | 440 | | | | | 445 | |
| 25 | AAA | GCC | AAA | GGG | CAG | CCC | CGA | GAA | CCA | CAG | GTG | TAC | ACC | CTG | CCC | CCA | 1056 |
| | Lys | Ala | Lys | Gly | Gln | Pro | Arg | Glu | Pro | Gln | Val | Tyr | Thr | Leu | Pro | Pro | |
| | | | | 450 | | | | | | 455 | | | | | 460 | | |
| 30 | TCC | CGG | GAT | GAG | CTG | ACC | AAG | AAC | CAG | GTC | AGC | CTG | ACC | TGC | CTG | GTC | 1104 |
| | Ser | Arg | Asp | Glu | Leu | Thr | Lys | Asn | Gln | Val | Ser | Leu | Thr | Cys | Leu | Val | |
| | | | | 465 | | | | | 470 | | | | | 475 | | | |
| 35 | AAA | GGC | TTC | TAT | CCC | AGC | GAC | ATC | GCC | GTG | GAG | TGG | GAG | AGC | AAT | GGG | 1152 |
| | Lys | Gly | Phe | Tyr | Pro | Ser | Asp | Ile | Ala | Val | Glu | Trp | Glu | Ser | Asn | Gly | |
| | | | 480 | | | | | 485 | | | | | 490 | | | | |
| 40 | CAG | CCG | GAG | AAC | AAC | TAC | AAG | ACC | ACG | CCT | CCC | GTG | CTG | GAC | TCC | GAC | 1200 |
| | Gln | Pro | Glu | Asn | Asn | Tyr | Lys | Thr | Thr | Pro | Pro | Val | Leu | Asp | Ser | Asp | |
| | | 495 | | | | | 500 | | | | | 505 | | | | | |
| 45 | GGC | TCC | TTC | TTC | CTC | TAC | AGC | AAG | CTC | ACC | GTG | GAC | AAG | AGC | AGG | TGG | 1248 |
| | Gly | Ser | Phe | Phe | Leu | Tyr | Ser | Lys | Leu | Thr | Val | Asp | Lys | Ser | Arg | Trp | |
| | 510 | | | | 515 | | | | | | 520 | | | | | 525 | |
| 50 | CAG | CAG | GGG | AAC | GTC | TTC | TCA | TGC | TCC | GTG | ATG | CAT | GAG | GCT | CTG | CAC | 1296 |
| | Gln | Gln | Gly | Asn | Val | Phe | Ser | Cys | Ser | Val | Met | His | Glu | Ala | Leu | His | |
| | | | | 530 | | | | | | 535 | | | | | 540 | | |
| 55 | AAC | CAC | TAC | ACG | CAG | AAG | AGC | CTC | TCC | CTG | TCT | CCG | GGT | AAA | | | 1338 |
| | Asn | His | Tyr | Thr | Gln | Lys | Ser | Leu | Ser | Leu | Ser | Pro | Gly | Lys | | | |
| | | | | 545 | | | | | 550 | | | | | 555 | | | |
| 50 | TGAGTGC | CGG | | | | | | | | | | | | | | | 1347 |

(2) INFORMATION FOR SEQ ID NO: 6:

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 6..23

(D) OTHER INFORMATION: This corresponds to Kinase
Primer 370-31.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

TCGTC GAC AAA ACT CAC ACA TGC C
Asp Lys Thr His Thr Cys
1 5

24

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: This corresponds to Kinase
Primer 370-32.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GTAAATGAGT GCGGCGGCCG CCAA

24

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GCGGCCGCGG TCCAACCACC AATCTCAAAG CTTGGTACCC GGGAATTCAG ATCTGCAGCA 60
 TGCTCGAGCT CTAGATATCG ATTCCATGGA TCCTCACATC CCAATCCGCG GCCGC 115

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(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 21..41

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GAGCTCGAGG CGGCCGCACC ATG CCT GGG AAG ATG GTC GTG 41
 Met Pro Gly Lys Met Val Val
 1 5

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(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

AAGTCGACTT GCAATTCTTT TAC 23

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(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TCGACGCGGC CGCG

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TCGACGCGGC CGCG